

SEQUENCE LISTING

<110> Li et al.

<120> G-Protein Receptor HTNAD29

<130> PF191D1C1

<150> US95/07288

<151> 1995-06-06

<150> 08/468,534

<151> 1995-06-06

<150> 09/399,095

<151> 1999-09-20

<160> 9

<170> PatentIn Version 3.1

<210> 1

<211> 1753

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (523)..(1533)

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attcatgttt gcaccaatct actgtgagat ttatgaagaa aaacaaattg cggacaactc      180
tctatgtaca cttacaaatg cctcagttga tgcttggtgg ctgtttgtca gcgttctgtg      240
ataatgaaca catggacttc tgtttattaa attcagttga cccctttagc caattgccag      300
gagcctggat ttttacttcc aactgctgat atctgtgtaa aaattgatct acatccaccc      360
tttaaaagca ttgatgaatt aattagaact ttagacaaca agaaaaattg aaaagaattc      420
tcagtaaaag cgaattcgat gttcaaaaca aactacaaag agacaagact tctctgttta      480
ctttctaaga actaatataa ttgctacctt aaaaaggaaa aa atg aac agc aca      534
                                     Met Asn Ser Thr
                                     1

tgt att gaa gaa cag cat gac ctg gat cac tat ttg ttt ccc att gtt      582
Cys Ile Glu Glu Gln His Asp Leu Asp His Tyr Leu Phe Pro Ile Val
5          10          15          20

tac atc ttt gtg att ata gtc agc att cca gcc aat att gga tct ctg      630
Tyr Ile Phe Val Ile Ile Val Ser Ile Pro Ala Asn Ile Gly Ser Leu

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25	30	35	
tgt gtg tct ttc ctg caa ccc aag aag gaa agt gaa cta gga att tac Cys Val Ser Phe Leu Gln Pro Lys Lys Glu Ser Glu Leu Gly Ile Tyr 40 45 50			678
ctc ttc agt ttg tca cta tca gat tta ctc tat gca tta act ctc cct Leu Phe Ser Leu Ser Leu Ser Asp Leu Leu Tyr Ala Leu Thr Leu Pro 55 60 65			726
tta tgg att gat tat act tgg aat aaa gac aac tgg act ttc tct cct Leu Trp Ile Asp Tyr Thr Trp Asn Lys Asp Asn Trp Thr Phe Ser Pro 70 75 80			774
gcc ttg tgc aaa ggg agt gct ttt ctc atg tac atg aag ttt tac agc Ala Leu Cys Lys Gly Ser Ala Phe Leu Met Tyr Met Lys Phe Tyr Ser 85 90 95 100			822
agc aca gca ttc ctc acc tgc att gcc gtt gat cgg tat ttg gct gtt Ser Thr Ala Phe Leu Thr Cys Ile Ala Val Asp Arg Tyr Leu Ala Val 105 110 115			870
gtc tac cct ttg aag ttt ttt ttc cta agg aca aga aga att gca ctc Val Tyr Pro Leu Lys Phe Phe Phe Leu Arg Thr Arg Arg Ile Ala Leu 120 125 130			918
atg gtc agc ctg tcc atc tgg ata ttg gaa acc atc ttc aat gct gtc Met Val Ser Leu Ser Ile Trp Ile Leu Glu Thr Ile Phe Asn Ala Val 135 140 145			966
atg ttg tgg gaa gat gaa aca gtt gtt gaa tat tgc gat gcc gaa aag Met Leu Trp Glu Asp Glu Thr Val Val Glu Tyr Cys Asp Ala Glu Lys 150 155 160			1014
tct aat ttt act tta tgc tat gac aaa tac cct tta gag aaa tgg caa Ser Asn Phe Thr Leu Cys Tyr Asp Lys Tyr Pro Leu Glu Lys Trp Gln 165 170 175 180			1062
atc aac ctc aac ttg ttc agg acg tgt aca ggc tat gca ata cct ttg Ile Asn Leu Asn Leu Phe Arg Thr Cys Thr Gly Tyr Ala Ile Pro Leu 185 190 195			1110
gtc acc atc ctg atc tgt aac cgg aaa gtc tac caa gct gtg cgg cac Val Thr Ile Leu Ile Cys Asn Arg Lys Val Tyr Gln Ala Val Arg His 200 205 210			1158
aat aaa gcc acg gaa aac aag gaa aag aag aga atc ata aaa cta ctt Asn Lys Ala Thr Glu Asn Lys Glu Lys Lys Arg Ile Ile Lys Leu Leu 215 220 225			1206
gtc agc atc aca gtt act ttt gtc tta tgc ttt act ccc ttt cat gtg Val Ser Ile Thr Val Thr Phe Val Leu Cys Phe Thr Pro Phe His Val 230 235 240			1254
atg ttg ctg att cgc tgc att tta gag cat gct gtg aac ttc gaa gac Met Leu Leu Ile Arg Cys Ile Leu Glu His Ala Val Asn Phe Glu Asp 245 250 255 260			1302
cac agc aat tct ggg aag cga act tac aca atg tat aga atc acg gtt			1350

His Ser Asn Ser Gly Lys Arg Thr Tyr Thr Met Tyr Arg Ile Thr Val
 265 270 275

gca tta aca agt tta aat tgt gtt gct gat cca att ctg tac tgt ttt 1398
 Ala Leu Thr Ser Leu Asn Cys Val Ala Asp Pro Ile Leu Tyr Cys Phe
 280 285 290

gtt acc gaa aca gga aga tat gat atg tgg aat ata tta aaa ttc tgc 1446
 Val Thr Glu Thr Gly Arg Tyr Asp Met Trp Asn Ile Leu Lys Phe Cys
 295 300 305

act ggg agg tgt aat aca tca caa aga caa aga aaa cgc ata ctt tct 1494
 Thr Gly Arg Cys Asn Thr Ser Gln Arg Gln Arg Lys Arg Ile Leu Ser
 310 315 320

gtg tct aca aaa gat act atg gaa tta gag gtc ctt gag tagaaccaag 1543
 Val Ser Thr Lys Asp Thr Met Glu Leu Glu Val Leu Glu
 325 330 335

gatgttttga agggaaggga agtttaagtt atgcattatt atatcatcaa gattacattt 1603

tgaaaaggaa atctagcatg tgaggggact aagtgttctc agagtgatgt tttaatccag 1663

tccaataaaaa atatcttaaaa actgcattgt acagctccct ccctgcggtt tattaaatga 1723

tgtatattaa acaaagatca atattttctt 1753

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 <213> Homo sapiens

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Ile Gly Ser Leu Cys Val Ser Phe Leu Gln Pro Lys Lys Glu Ser Glu
 35 40 45

Leu Gly Ile Tyr Leu Phe Ser Leu Ser Leu Ser Asp Leu Leu Tyr Ala
 50 55 60

Leu Thr Leu Pro Leu Trp Ile Asp Tyr Thr Trp Asn Lys Asp Asn Trp
 65 70 75 80

Thr Phe Ser Pro Ala Leu Cys Lys Gly Ser Ala Phe Leu Met Tyr Met
 85 90 95

Lys Phe Tyr Ser Ser Thr Ala Phe Leu Thr Cys Ile Ala Val Asp Arg
100 105 110

Tyr Leu Ala Val Val Tyr Pro Leu Lys Phe Phe Phe Leu Arg Thr Arg
115 120 125

Arg Ile Ala Leu Met Val Ser Leu Ser Ile Trp Ile Leu Glu Thr Ile
130 135 140

Phe Asn Ala Val Met Leu Trp Glu Asp Glu Thr Val Val Glu Tyr Cys
145 150 155 160

Asp Ala Glu Lys Ser Asn Phe Thr Leu Cys Tyr Asp Lys Tyr Pro Leu
165 170 175

Glu Lys Trp Gln Ile Asn Leu Asn Leu Phe Arg Thr Cys Thr Gly Tyr
180 185 190

Ala Ile Pro Leu Val Thr Ile Leu Ile Cys Asn Arg Lys Val Tyr Gln
195 200 205

Ala Val Arg His Asn Lys Ala Thr Glu Asn Lys Glu Lys Lys Arg Ile
210 215 220

Ile Lys Leu Leu Val Ser Ile Thr Val Thr Phe Val Leu Cys Phe Thr
225 230 235 240

Pro Phe His Val Met Leu Leu Ile Arg Cys Ile Leu Glu His Ala Val
245 250 255

Asn Phe Glu Asp His Ser Asn Ser Gly Lys Arg Thr Tyr Thr Met Tyr
260 265 270

Arg Ile Thr Val Ala Leu Thr Ser Leu Asn Cys Val Ala Asp Pro Ile
275 280 285

Leu Tyr Cys Phe Val Thr Glu Thr Gly Arg Tyr Asp Met Trp Asn Ile
290 295 300

Leu Lys Phe Cys Thr Gly Arg Cys Asn Thr Ser Gln Arg Gln Arg Lys
305 310 315 320

Arg Ile Leu Ser Val Ser Thr Lys Asp Thr Met Glu Leu Glu Val Leu
325 330 335

Glu

<210> 3
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<212> PRT
<213> Homo sapiens

<400> 3

Asp Ser Ser His Met Asp Ser Glu Phe Arg Tyr Thr Leu Phe Pro Ile
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Val Tyr Ser Ile Ile Phe Val Leu Gly Val Ile Ala Asn Gly Tyr Val
20 25 30

Leu Trp Val Phe Ala Arg Leu Tyr Pro Cys Lys Lys Phe Asn Glu Ile
35 40 45

Lys Ile Phe Met Val Asn Leu Thr Met Ala Asp Met Leu Phe Leu Ile
50 55 60

Thr Leu Pro Leu Trp Ile Val Tyr Tyr Gln Asn Gln Gly Asn Trp Ile
65 70 75 80

Leu Pro Lys Phe Leu Cys Asn Val Ala Gly Cys Leu Phe Phe Ile Asn
85 90 95

Thr Tyr Cys Ser Val Ala Phe Leu Gly Val Ile Thr Tyr Asn Arg Phe
100 105 110

Gln Ala Val Thr Arg Pro Ile Lys Thr Ala Gln Ala Asn Thr Arg Lys
115 120 125

Arg Gly Ile Ser Leu Ser Leu Val Ile Trp Val Ala Ile Val Gly Ala
130 135 140

Ala Ser Tyr Phe Leu Ile Leu Asp Ser Thr Asn Thr Val Pro Asp Ser
145 150 155 160

Ala Gly Ser Gly Asn Val Thr Arg Cys Phe Glu His Tyr Glu Lys Gly
165 170 175

Ser Val Pro Val Leu Ile Ile His Ile Phe Ile Val Phe Ser Phe Phe
180 185 190

Leu Val Phe Leu Ile Ile Leu Phe Cys Asn Leu Val Ile Ile Arg Thr
 195 200 205

Leu Leu Met Gln Pro Val Gln Gln Gln Arg Asn Ala Glu Val Thr Gly
 210 215 220

Arg Ala Leu Trp Met Val Cys Thr Val Leu Ala Val Phe Ile Ile Cys
 225 230 235 240

Phe Val Pro His His Val Val Gln Leu Pro Trp Thr Leu Ala Glu Leu
 245 250 255

Gly Phe Gln Asp Ser Lys Phe His Gln Ala Ile Asn Asp Ala His Gln
 260 265 270

Val Thr Leu Cys Leu Leu Ser Thr Asn Cys Val Leu Asp Pro Val Ile
 275 280 285

Tyr Cys Phe Leu Thr Lys Lys Phe Arg Lys His Leu Thr Glu Lys Phe
 290 295 300

Tyr Ser Met Arg Ser Ser Arg Lys Cys Ser Arg Ala Thr Thr Asp Thr
 305 310 315 320

Val Thr Glu Val Val Val Pro
 325

<210> 4
 <211> 29
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Contains an EcoRI restriction enzyme site

<400> 4
 cgaattcctc catgaacagc acatgtatt

29

<210> 5
 <211> 29
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Contains complementary sequences to a HindIII site

<400> 5
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29

<210> 6
 <211> 34
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Contains a HindIII site

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<210> 7
 <211> 61
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Contains complementary sequences to an XhoI site,
 translation stop codon, and an HA tag

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60

a

61

<210> 8
 <211> 30
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Contains a BamHI restriction enzyme site followed by 4
 nucleotides resembling an efficient signal for the initiation
 of translation in eukaryotic cells

<400> 8
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30

<210> 9
 <211> 32
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Contains the cleavage site for the restriction
 endonuclease BamHI

<400> 9
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32